AU 1812

INPUT SET: S12354.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

```
 1                            SEQUENCE LISTING
 2
 3   (1)    General Information:
 4
 5     (i)  APPLICANT: Eaton, Dan L.
 6                     de Sauvage, Frederic J.         ENTERED
 7
 8    (ii)  TITLE OF INVENTION: HUMAN MPL LIGAND
 9
10   (iii)  NUMBER OF SEQUENCES: 30
11
12    (iv)  CORRESPONDENCE ADDRESS:
13          (A) ADDRESSEE: Genentech, Inc.
14          (B) STREET: 460 Point San Bruno Blvd
15          (C) CITY: South San Francisco
16          (D) STATE: California
17          (E) COUNTRY: USA
18          (F) ZIP: 94080
19
20     (v)  COMPUTER READABLE FORM:
21          (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
22          (B) COMPUTER: IBM PC compatible
23          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24          (D) SOFTWARE: WinPatin (Genentech)
25
26    (vi)  CURRENT APPLICATION DATA:
27          (A) APPLICATION NUMBER: 08/223263
28          (B) FILING DATE: 04-Apr-1994
29          (C) CLASSIFICATION:
30
31   (vii)  PRIOR APPLICATION DATA:
32          (A) APPLICATION NUMBER: 08/196689
33          (B) FILING DATE: 15-FEB-1994
34
35   (vii)  PRIOR APPLICATION DATA:
36          (A) APPLICATION NUMBER: 08/185607
37          (B) FILING DATE: 21-JAN-1994
38
39   (vii)  PRIOR APPLICATION DATA:
40          (A) APPLICATION NUMBER: 08/176553
41          (B) FILING DATE: 3-JAN-1994
42
43  (viii)  ATTORNEY/AGENT INFORMATION:
44          (A) NAME: Winter, Daryl B.
45          (B) REGISTRATION NUMBER: 32,637
46          (C) REFERENCE/DOCKET NUMBER: P0871P3
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47
48        (ix) TELECOMMUNICATION INFORMATION:
49              (A) TELEPHONE: 415/225-1249
50              (B) TELEFAX: 415/952-9881
51              (C) TELEX: 910/371-7168
52
53    (2) INFORMATION FOR SEQ ID NO:1:
54
55        (i) SEQUENCE CHARACTERISTICS:
56              (A) LENGTH: 353 amino acids
57              (B) TYPE: Amino Acid
58              (D) TOPOLOGY: Linear
59
60        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
61
62    Met Glu Leu Thr Glu Leu Leu Val Val Met Leu Leu Leu Thr
63    -21 -20            -15             -10
64
65    Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu
66        -5              1               5
67
68    Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser
69    10              15              20
70
71    Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
72    25              30              35
73
74    Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
75    40              45              50
76
77    Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu
78    55              60              65
79
80    Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
81    70              75              80
82
83    Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
84    85              90              95
85
86    Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro
87    100             105             110
88
89    Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu
90    115             120             125
91
92    Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu
93    130             135             140
94
95    Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr
96    145             150             155
97
98    Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu
99    160             165             170
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100
101    Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr Ala Ser
102    175             180             185
103
104    Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly Phe
105    190             195             200
106
107    Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu
108    205             210             215
109
110    Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn
111    220             225             230
112
113    Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly
114    235             240             245
115
116    Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro
117    250             255             260
118
119    Pro Asn Leu Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro
120    265             270             275
121
122    Thr Gly Gln Tyr Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr
123    280             285             290
124
125    Pro Val Val Gln Leu His Pro Leu Leu Pro Asp Pro Ser Ala Pro
126    295             300             305
127
128    Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His
129    310             315             320
130
131    Ser Gln Asn Leu Ser Gln Glu Gly
132    325             330     332
133
134    (2) INFORMATION FOR SEQ ID NO:2:
135
136       (i) SEQUENCE CHARACTERISTICS:
137           (A) LENGTH: 1795 base pairs
138           (B) TYPE: Nucleic Acid
139           (C) STRANDEDNESS: Single
140           (D) TOPOLOGY: Linear
141
142      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
143
144
145    TCTTCCTACC CATCTGCTCC CCAGAGGGCT GCCTGCTGTG CACTTGGGTC 50
146
147    CTGGAGCCCT TCTCCACCCG GATAGATTCC TCACCCTTGG CCCGCCTTTG 100
148
149    CCCCACCCTA CTCTGCCCAG AAGTGCAAGA GCCTAAGCCG CCTCCATGGC 150
150
151    CCCAGGAAGG ATTCAGGGGA GAGGCCCCAA ACAGGGAGCC ACGCCAGCCA 200
152
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INPUT SET: S12354.raw

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153    GACACCCCGG CCAGA      ATG GAG CTG ACT GAA TTG CTC CTC 239
154                         Met Glu Leu Thr Glu Leu Leu Leu
155                         -21 -20                  -15

156
157    GTG GTC ATG CTT CTC CTA ACT GCA AGG CTA ACG CTG TCC 278
158    Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu Ser
159            -10                  -5

160
161    AGC CCG GCT CCT CCT GCT TGT GAC CTC CGA GTC CTC AGT 317
162    Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser
163     1           5                   10

164
165    AAA CTG CTT CGT GAC TCC CAT GTC CTT CAC AGC AGA CTG 356
166    Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu
167         15              20                  25

168
169    AGC CAG TGC CCA GAG GTT CAC CCT TTG CCT ACA CCT GTC 395
170    Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
171             30                  35

172
173    CTG CTG CCT GCT GTG GAC TTT AGC TTG GGA GAA TGG AAA 434
174    Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys
175     40              45                  50

176
177    ACC CAG ATG GAG GAG ACC AAG GCA CAG GAC ATT CTG GGA 473
178    Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly
179             55                  60                  65

180
181    GCA GTG ACC CTT CTG CTG GAG GGA GTG ATG GCA GCA CGG 512
182    Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg
183                 70                  75

184
185    GGA CAA CTG GGA CCC ACT TGC CTC TCA TCC CTC CTG GGG 551
186    Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly
187         80                  85                  90

188
189    CAG CTT TCT GGA CAG GTC CGT CTC CTC CTT GGG GCC CTG 590
190    Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu
191             95                  100

192
193    CAG AGC CTC CTT GGA ACC CAG CTT CCT CCA CAG GGC AGG 629
194    Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg
195    105                  110                  115

196
197    ACC ACA GCT CAC AAG GAT CCC AAT GCC ATC TTC CTG AGC 668
198    Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu Ser
199             120                  125                  130

200
201    TTC CAA CAC CTG CTC CGA GGA AAG GTG CGT TTC CTG ATG 707
202    Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met
203             135                  140

204
205    CTT GTA GGA GGG TCC ACC CTC TGC GTC AGG CGG GCC CCA 746
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INPUT SET: S12354.raw

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206   Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro
207       145                 150                 155
208
209   CCC ACC ACA GCT GTC CCC AGC AGA ACC TCT CTA GTC CTC 785
210   Pro Thr Thr Ala Val Pro Ser Arg Thr Ser Leu Val Leu
211           160                 165
212
213   ACA CTG AAC GAG CTC CCA AAC AGG ACT TCT GGA TTG TTG 824
214   Thr Leu Asn Glu Leu Pro Asn Arg Thr Ser Gly Leu Leu
215   170                 175                 180
216
217   GAG ACA AAC TTC ACT GCC TCA GCC AGA ACT ACT GGC TCT 863
218   Glu Thr Asn Phe Thr Ala Ser Ala Arg Thr Thr Gly Ser
219           185                 190                 195
220
221   GGG CTT CTG AAG TGG CAG CAG GGA TTC AGA GCC AAG ATT 902
222   Gly Leu Leu Lys Trp Gln Gln Gly Phe Arg Ala Lys Ile
223               200                 205
224
225   CCT GGT CTG CTG AAC CAA ACC TCC AGG TCC CTG GAC CAA 941
226   Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu Asp Gln
227       210                 215                 220
228
229   ATC CCC GGA TAC CTG AAC AGG ATA CAC GAA CTC TTG AAT 980
230   Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn
231               225                 230
232
233   GGA ACT CGT GGA CTC TTT CCT GGA CCC TCA CGC AGG ACC 1019
234   Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr
235   235                 240                 245
236
237   CTA GGA GCC CCG GAC ATT TCC TCA GGA ACA TCA GAC ACA 1058
238   Leu Gly Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr
239           250                 255                 260
240
241   GGC TCC CTG CCA CCC AAC CTC CAG CCT GGA TAT TCT CCT 1097
242   Gly Ser Leu Pro Pro Asn Leu Gln Pro Gly Tyr Ser Pro
243               265                 270
244
245   TCC CCA ACC CAT CCT CCT ACT GGA CAG TAT ACG CTC TTC 1136
246   Ser Pro Thr His Pro Pro Thr Gly Gln Tyr Thr Leu Phe
247       275                 280                 285
248
249   CCT CTT CCA CCC ACC TTG CCC ACC CCT GTG GTC CAG CTC 1175
250   Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu
251           290                 295
252
253   CAC CCC CTG CTT CCT GAC CCT TCT GCT CCA ACG CCC ACC 1214
254   His Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr
255   300                 305                 310
256
257   CCT ACC AGC CCT CTT CTA AAC ACA TCC TAC ACC CAC TCC 1253
258   Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His Ser
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/223,263A*

INPUT SET: S12354.raw

Line	Error	Original Text
27	Wrong application Serial Number	(A) APPLICATION NUMBER: 08/223263